

# SEQ SEARCH SUMMARY

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 4, 2004, 20:02:20 ; Search time 8051 Seconds  
(without alignments)  
2756.382 Million cell updates/sec

Title: US-09-743-209A-2  
Perfect score: 2618  
Sequence: 1 GAPVLPAAFGFLASARTGGG.....EVDTDVVRSVADRTARGAA 512

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlp

Q=/cgn2\_1/USPTO\_spool\_p/US09743209/runat\_02062004\_111815\_22096/app\_query.fasta\_1.711

-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09743209\_@CGN\_1\_1\_7406\_@runat\_02062004\_111815\_22096 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*

11: gb\_sts:\*  
 12: gb\_sy:\*  
 13: gb\_un:\*  
 14: gb\_vi:\*  
 15: em\_ba:\*  
 16: em\_fun:\*  
 17: em\_hum:\*  
 18: em\_in:\*  
 19: em\_mu:\*  
 20: em\_om:\*  
 21: em\_or:\*  
 22: em\_ov:\*  
 23: em\_pat:\*  
 24: em\_ph:\*  
 25: em\_pl:\*  
 26: em\_ro:\*  
 27: em\_sts:\*  
 28: em\_un:\*  
 29: em\_vi:\*  
 30: em\_htg\_hum:\*  
 31: em\_htg\_inv:\*  
 32: em\_htg\_other:\*  
 33: em\_htg\_mus:\*  
 34: em\_htg\_pln:\*  
 35: em\_htg\_rod:\*  
 36: em\_htg\_mam:\*  
 37: em\_htg\_vrt:\*  
 38: em\_sy:\*  
 39: em\_htgo\_hum:\*  
 40: em\_htgo\_mus:\*  
 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID                     | Description                    |
|------------|-------|---------|--------------|----|------------------------|--------------------------------|
| 1          | 2618  | 100.0   | 1542         | 1  | AF071051-GB 8/15/98    | AF071051 Streptomy             |
| 2          | 2618  | 100.0   | 1542         | 6  | AR151707 USPN 6232106  | AR151707 Sequence              |
| 3          | 2618  | 100.0   | 1542         | 6  | AR352528 6589775       | AR352528 Sequence              |
| 4          | 2618  | 100.0   | 1542         | 6  | AX006515 WO 00/03581   | AX006515 Sequence Appl.        |
| 5          | 2618  | 100.0   | 1542         | 6  | BD217691 JP 2002520033 | BD217691 Process f             |
| 6          | 2618  | 100.0   | 11604        | 6  | AR151704               | AR151704 Sequence              |
| 7          | 2618  | 100.0   | 11604        | 6  | AR352525               | AR352525 Sequence              |
| 8          | 2618  | 100.0   | 15079        | 6  | AR151702               | AR151702 Sequence              |
| 9          | 2618  | 100.0   | 15120        | 1  | SCU87786-GB 3/6/98     | U87786 Streptomyce             |
| 10         | 2618  | 100.0   | 15120        | 6  | AR352523               | AR352523 Sequence              |
| 11         | 2618  | 100.0   | 29870        | 6  | AX763606 WO 03/040372  | AX763606 Sequence              |
| 12         | 2229  | 85.1    | 6584         | 1  | SCPAHCAS               | GB-X84101 S.clavulige-fragment |
| c 13       | 1051  | 40.1    | 5945         | 1  | AY426768               | AY426768 Streptomy             |
| c 14       | 420.5 | 16.1    | 32329        | 1  | SCA421798              | AJ421798 Streptomy             |
| c 15       | 363   | 13.9    | 10481        | 1  | AE013530               | AE013530 Methanosa             |
| 16         | 348   | 13.3    | 10029        | 1  | AE010880               | AE010880 Methanosa             |

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 4, 2004, 18:56:39 ; Search time 748 Seconds  
(without alignments)  
2907.858 Million cell updates/sec

Title: US-09-743-209A-2  
Perfect score: 2618  
Sequence: 1 GAPVLPAAFGFLASARTGGG.....EVDTDVVRVSVADRTARGAA 512

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlp

Q=/cgn2\_1/USPTO\_spool\_p/US09743209/runat\_02062004\_111815\_22059/app\_query.fasta\_1  
.711

-DB=N\_Geneseq\_29Jan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09743209@CGN\_1\_1\_885@runat\_02062004\_111815\_22059 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Geneseq\_29Jan04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002s:\*  
7: geneseqn2003as:\*  
8: geneseqn2003bs:\*  
9: geneseqn2003cs:\*  
10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result | No. | Score | %<br>Query Match | Length | DB | ID       | Description        |
|--------|-----|-------|------------------|--------|----|----------|--------------------|
|        | 1   | 2618  | 100.0            | 1542   | 3  | AAZ60717 | Aaz60717 DNA encod |
|        | 2   | 2618  | 100.0            | 1542   | 4  | AAD14504 | Aad14504 S. clavul |
|        | 3   | 2618  | 100.0            | 1542   | 7  | ACA62927 | Aca62927 DNA encod |
|        | 4   | 2618  | 100.0            | 1542   | 9  | ADD26445 | Add26445 Streptomy |
|        | 5   | 2618  | 100.0            | 11604  | 4  | AAD14501 | Aad14501 Streptomy |
|        | 6   | 2618  | 100.0            | 11604  | 7  | ACA62924 | Aca62924 Clavulani |
|        | 7   | 2618  | 100.0            | 11604  | 9  | ADD26442 | Add26442 Streptomy |
|        | 8   | 2618  | 100.0            | 15079  | 2  | AAQ91580 | Aaq91580 S. clavul |
|        | 9   | 2618  | 100.0            | 15079  | 4  | AAD14499 | Aad14499 Streptomy |
|        | 10  | 2618  | 100.0            | 15079  | 7  | ACA62922 | Aca62922 Streptomy |
|        | 11  | 2618  | 100.0            | 15120  | 9  | ADD26455 | Add26455 Streptomy |
|        | 12  | 2618  | 100.0            | 29870  | 7  | AAD36874 | Aad36874 Streptomy |
|        | 13  | 330   | 12.6             | 8341   | 2  | AAT09700 | Aat09700 DNA encod |
|        | 14  | 274   | 10.5             | 1956   | 7  | ACA38291 | Aca38291 Prokaryot |
| c      | 15  | 273.5 | 10.4             | 40138  | 2  | AAV81946 | Aav81946 V. marinu |
| c      | 16  | 273.5 | 10.4             | 40138  | 3  | AAA71520 | Aaa71520 V. marinu |
| c      | 17  | 273.5 | 10.4             | 41587  | 4  | AAI64984 | Aai64984 Moritella |
|        | 18  | 271   | 10.4             | 1959   | 7  | ACA40616 | Aca40616 Prokaryot |
|        | 19  | 271   | 10.4             | 110000 | 4  | AAI99682 | Continuation (25 o |
|        | 20  | 271   | 10.4             | 110000 | 4  | AAI99683 | Continuation (25 o |
|        | 21  | 265.5 | 10.1             | 1770   | 7  | ACA42428 | Aca42428 Prokaryot |
|        | 22  | 263   | 10.0             | 1506   | 7  | ACF70233 | Acf70233 Photorhab |
| c      | 23  | 263   | 10.0             | 110000 | 7  | ACF65385 | Continuation (4 of |
| c      | 24  | 263   | 10.0             | 110000 | 7  | ACF65385 | Continuation (5 of |
| c      | 25  | 263   | 10.0             | 110000 | 7  | ACF67367 | Continuation (34 o |
|        | 26  | 258   | 9.9              | 1929   | 7  | ACA37874 | Aca37874 Prokaryot |
|        | 27  | 257.5 | 9.8              | 1866   | 7  | ACA26323 | Aca26323 Prokaryot |
|        | 28  | 251.5 | 9.6              | 1863   | 7  | ABT32130 | Abt32130 Benzodiaz |
| c      | 29  | 251.5 | 9.6              | 32539  | 7  | ABT32129 | Abt32129 Benzodiaz |
|        | 30  | 245.5 | 9.4              | 1773   | 7  | ADA71087 | Ada71087 Rice gene |
|        | 31  | 238.5 | 9.1              | 58857  | 3  | AAA58471 | Aaa58471 Nucleotid |
|        | 32  | 237   | 9.1              | 1803   | 7  | ACA37755 | Aca37755 Prokaryot |
|        | 33  | 237   | 9.1              | 1962   | 7  | ACA23550 | Aca23550 Prokaryot |
|        | 34  | 235   | 9.0              | 1533   | 7  | ACF67631 | Acf67631 Photorhab |
| c      | 35  | 235   | 9.0              | 110000 | 7  | ACF65383 | Continuation (2 of |
| c      | 36  | 235   | 9.0              | 110000 | 7  | ACF67367 | Continuation (3 of |
|        | 37  | 233   | 8.9              | 1665   | 7  | ACA51672 | Aca51672 Prokaryot |
|        | 38  | 232.5 | 8.9              | 1836   | 3  | AAC46946 | Aac46946 Arabidops |
|        | 39  | 232   | 8.9              | 1665   | 7  | ACA32421 | Aca32421 Prokaryot |
|        | 40  | 231   | 8.8              | 1959   | 7  | ACA26531 | Aca26531 Prokaryot |
|        | 41  | 229.5 | 8.8              | 1872   | 4  | AAF77894 | Aaf77894 Quorum se |
|        | 42  | 229.5 | 8.8              | 2034   | 7  | ACA39722 | Aca39722 Prokaryot |
|        | 43  | 227   | 8.7              | 1662   | 7  | ACA35379 | Aca35379 Prokaryot |
|        | 44  | 227   | 8.7              | 1788   | 7  | ACA45735 | Aca45735 Prokaryot |
| c      | 45  | 226   | 8.6              | 30001  | 2  | AAT61016 | Aat61016 Total DNA |

# ALIGNMENTS

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 4, 2004, 14:00:59 ; Search time 119 Seconds  
(without alignments)  
2387.688 Million cell updates/sec

Title: US-09-743-209A-2  
Perfect score: 2618  
Sequence: 1 GAPVLPAAFGFLASARTGGG.....EVDTTDDVVRVSVADRTARGAA 512

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlp

Q=/cg2\_1/USPTO\_spool\_p/US09743209/runat\_02062004\_111813\_21989/app\_query.fasta\_1  
.711

-DB=Issued\_Patents\_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09743209 @CGN\_1\_1\_128 @runat\_02062004\_111813\_21989 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued\_Patents\_NA:\*  
1: /cg2\_6/ptodata/2/ina/5A\_COMB.seq:\*  
2: /cg2\_6/ptodata/2/ina/5B\_COMB.seq:\*  
3: /cg2\_6/ptodata/2/ina/6A\_COMB.seq:\*  
4: /cg2\_6/ptodata/2/ina/6B\_COMB.seq:\*  
5: /cg2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*  
6: /cg2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result<br>No. | %     |       | Query   |    |                      | ID | Description        |
|---------------|-------|-------|---------|----|----------------------|----|--------------------|
|               | Score | Match | Length  | DB |                      |    |                    |
| 1             | 2618  | 100.0 | 1542    | 3  | US-09-385-028-16     | ✓  | Sequence 16, Appl  |
| 2             | 2618  | 100.0 | 1542    | 4  | US-09-726-614-16     | ✓  | Sequence 16, Appl  |
| 3             | 2618  | 100.0 | 1542    | 4  | US-09-385-040-16     | ✓  | Sequence 16, Appl  |
| 4             | 2618  | 100.0 | 11604   | 3  | US-09-385-028-13     |    | Sequence 13, Appl  |
| 5             | 2618  | 100.0 | 11604   | 4  | US-09-726-614-13     |    | Sequence 13, Appl  |
| 6             | 2618  | 100.0 | 11604   | 4  | US-09-385-040-13     |    | Sequence 13, Appl  |
| 7             | 2618  | 100.0 | 15079   | 3  | US-09-385-028-1      |    | Sequence 1, Appli  |
| 8             | 2618  | 100.0 | 15079   | 4  | US-09-726-614-1      |    | Sequence 1, Appli  |
| 9             | 2618  | 100.0 | 15120   | 4  | US-09-385-040-1      |    | Sequence 1, Appli  |
| 10            | 330   | 12.6  | 8341    | 2  | US-08-737-825-1      |    | Sequence 1, Appli  |
| c 11          | 273.5 | 10.4  | 40138   | 3  | US-09-090-793-12     |    | Sequence 12, Appl  |
| c 12          | 273.5 | 10.4  | 40138   | 4  | US-09-231-899-12     |    | Sequence 12, Appl  |
| 13            | 271   | 10.4  | 4403765 | 3  | US-09-103-840A-2     |    | Sequence 2, Appli  |
| 14            | 271   | 10.4  | 4411529 | 3  | US-09-103-840A-1     |    | Sequence 1, Appli  |
| 15            | 265.5 | 10.1  | 1944    | 4  | US-09-252-991A-889   |    | Sequence 889, App  |
| 16            | 236   | 9.0   | 2067    | 4  | US-09-252-991A-16177 |    | Sequence 16177, A  |
| c 17          | 226   | 8.6   | 30001   | 1  | US-08-125-468-1      |    | Sequence 1, Appli  |
| c 18          | 226   | 8.6   | 30001   | 2  | US-08-474-933-1      |    | Sequence 1, Appli  |
| 19            | 209.5 | 8.0   | 1635    | 4  | US-09-489-039A-5962  |    | Sequence 5962, Ap  |
| 20            | 209   | 8.0   | 1920    | 4  | US-09-252-991A-8518  |    | Sequence 8518, Ap  |
| c 21          | 204.5 | 7.8   | 2013    | 4  | US-09-252-991A-8359  |    | Sequence 8359, Ap  |
| 22            | 204.5 | 7.8   | 2409    | 4  | US-09-252-991A-8479  |    | Sequence 8479, Ap  |
| 23            | 203   | 7.8   | 2002    | 6  | 5256558-3            |    | Patent No. 5256558 |
| 24            | 188.5 | 7.2   | 1886    | 6  | 5256558-1            |    | Patent No. 5256558 |
| 25            | 187   | 7.1   | 1992    | 4  | US-09-220-132-55     |    | Sequence 55, Appl  |
| c 26          | 186   | 7.1   | 1368    | 4  | US-09-252-991A-1071  |    | Sequence 1071, Ap  |
| 27            | 174   | 6.6   | 1664976 | 4  | US-08-916-421B-1     |    | Sequence 1, Appli  |
| 28            | 171.5 | 6.6   | 43280   | 2  | US-08-804-227C-1     |    | Sequence 1, Appli  |
| 29            | 170   | 6.5   | 33529   | 3  | US-09-144-085-3      |    | Sequence 3, Appli  |
| 30            | 166   | 6.3   | 1446    | 4  | US-09-252-991A-5355  |    | Sequence 5355, Ap  |
| 31            | 154   | 5.9   | 44377   | 2  | US-08-804-227C-7     |    | Sequence 7, Appli  |
| 32            | 154   | 5.9   | 44377   | 2  | US-08-804-198-1      |    | Sequence 1, Appli  |
| 33            | 151.5 | 5.8   | 10023   | 4  | US-09-252-991A-6997  |    | Sequence 6997, Ap  |
| 34            | 151   | 5.8   | 1896    | 4  | US-09-107-532A-2923  |    | Sequence 2923, Ap  |
| c 35          | 149   | 5.7   | 4403765 | 3  | US-09-103-840A-2     |    | Sequence 2, Appli  |
| c 36          | 149   | 5.7   | 4411529 | 3  | US-09-103-840A-1     |    | Sequence 1, Appli  |
| 37            | 148.5 | 5.7   | 4425    | 1  | US-08-222-616-32     |    | Sequence 32, Appl  |
| 38            | 148.5 | 5.7   | 4425    | 4  | US-08-446-648-32     |    | Sequence 32, Appl  |
| 39            | 148.5 | 5.7   | 4425    | 4  | US-09-982-610-32     |    | Sequence 32, Appl  |
| 40            | 148.5 | 5.7   | 4425    | 5  | PCT-US95-04228-32    |    | Sequence 32, Appl  |
| 41            | 144.5 | 5.5   | 71989   | 4  | US-09-443-501A-2     |    | Sequence 2, Appli  |
| 42            | 144   | 5.5   | 2409    | 4  | US-09-252-991A-1259  |    | Sequence 1259, Ap  |
| c 43          | 142.5 | 5.4   | 77536   | 4  | US-09-410-551B-1     |    | Sequence 1, Appli  |
| 44            | 142   | 5.4   | 77536   | 4  | US-09-410-551B-1     |    | Sequence 1, Appli  |
| c 45          | 140.5 | 5.4   | 2022    | 4  | US-09-252-991A-8890  |    | Sequence 8890, Ap  |

## ALIGNMENTS

## RESULT 1

US-09-385-028-16

; Sequence 16, Application US/09385028

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 4, 2004, 17:14:45 ; Search time 784 Seconds  
(without alignments)  
2979.263 Million cell updates/sec

Title: US-09-743-209A-2  
Perfect score: 2618  
Sequence: 1 GAPVLPAAFGFLASARTGGG.....EVDTTDDVVRSVADRTARGAA 512

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2995936 seqs, 2280998010 residues

Total number of hits satisfying chosen parameters: 5991872

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+\_p2n.model -DEV=xlp

Q=/cgn2\_1/USPTO\_spool\_p/US09743209/runat\_02062004\_111814\_22028/app\_query.fasta\_1  
.711  
-DB=Published\_Applications\_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US09743209 @CGN\_1\_1\_912 @runat\_02062004\_111814\_22028  
-NCPU=6 -ICPU=3 -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published\_Applications\_NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*

12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
 13: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq2:\*  
 14: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*  
 15: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*  
 16: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*  
 17: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
 18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
 19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | %           |        | DB    | ID | Description          |
|------------|-------|-------------|--------|-------|----|----------------------|
|            |       | Query Match | Length |       |    |                      |
|            | 1     | 2618        | 100.0  | 1542  | 16 | US-10-458-201-16✓    |
|            | 2     | 2618        | 100.0  | 11604 | 16 | US-10-458-201-13✓    |
|            | 3     | 2618        | 100.0  | 15120 | 16 | US-10-458-201-1✓     |
| c          | 4     | 420.5       | 16.1   | 32329 | 13 | US-10-374-903A-1     |
|            | 5     | 281.5       | 10.8   | 2120  | 13 | US-10-425-114-25288  |
|            | 6     | 278.5       | 10.6   | 2132  | 13 | US-10-425-114-35023  |
|            | 7     | 274         | 10.5   | 1956  | 13 | US-10-282-122A-26161 |
| c          | 8     | 273.5       | 10.4   | 40138 | 15 | US-10-331-061-12     |
|            | 9     | 271         | 10.4   | 1959  | 13 | US-10-282-122A-28486 |
|            | 10    | 269         | 10.3   | 1971  | 13 | US-10-425-114-21636  |
|            | 11    | 269         | 10.3   | 1990  | 13 | US-10-425-114-22644  |
|            | 12    | 265.5       | 10.1   | 1770  | 13 | US-10-282-122A-30298 |
|            | 13    | 259.5       | 9.9    | 2080  | 13 | US-10-425-114-13515  |
|            | 14    | 259.5       | 9.9    | 2080  | 13 | US-10-425-114-17231  |
|            | 15    | 259.5       | 9.9    | 2115  | 13 | US-10-425-114-33954  |
|            | 16    | 259.5       | 9.9    | 2162  | 13 | US-10-425-114-29113  |
|            | 17    | 259.5       | 9.9    | 2178  | 13 | US-10-425-114-22140  |
|            | 18    | 258         | 9.9    | 1929  | 13 | US-10-282-122A-25744 |
|            | 19    | 257.5       | 9.8    | 1866  | 13 | US-10-282-122A-14193 |
|            | 20    | 251.5       | 9.6    | 1863  | 15 | US-10-166-087-3      |
| c          | 21    | 251.5       | 9.6    | 32539 | 15 | US-10-166-087-1      |
|            | 22    | 245         | 9.4    | 2121  | 13 | US-10-425-114-24843  |
|            | 23    | 245         | 9.4    | 2199  | 13 | US-10-425-114-28820  |
|            | 24    | 245         | 9.4    | 2228  | 13 | US-10-425-114-29114  |
|            | 25    | 245         | 9.4    | 2248  | 13 | US-10-425-114-1380   |
|            | 26    | 244         | 9.3    | 2155  | 13 | US-10-425-114-28232  |
|            | 27    | 244         | 9.3    | 2159  | 13 | US-10-425-114-24881  |
|            | 28    | 244         | 9.3    | 2168  | 13 | US-10-425-114-28007  |
|            | 29    | 244         | 9.3    | 2172  | 13 | US-10-425-114-26770  |
|            | 30    | 244         | 9.3    | 2175  | 13 | US-10-425-114-24463  |
|            | 31    | 244         | 9.3    | 2175  | 13 | US-10-425-114-24505  |
|            | 32    | 244         | 9.3    | 2181  | 13 | US-10-425-114-24584  |
|            | 33    | 244         | 9.3    | 2182  | 13 | US-10-425-114-28805  |
|            | 34    | 237         | 9.1    | 1803  | 13 | US-10-282-122A-25625 |
|            | 35    | 237         | 9.1    | 1962  | 13 | US-10-282-122A-11420 |
|            | 36    | 233         | 8.9    | 1665  | 13 | US-10-282-122A-39542 |
| c          | 37    | 232.5       | 8.9    | 85692 | 17 | US-10-461-194-1      |
|            | 38    | 232         | 8.9    | 1665  | 13 | US-10-282-122A-20291 |
|            | 39    | 232         | 8.9    | 2183  | 13 | US-10-424-599-54780  |



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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 4, 2004, 20:42:00 ; Search time 4976 Seconds  
(without alignments)  
3072.636 Million cell updates/sec

Title: US-09-743-209A-2  
Perfect score: 2618  
Sequence: 1 GAPVLPAAFGFLASARTGGG.....EVDTDVVRSVADRTARGAA 512

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+\_p2n.model -DEV=xlp

Q=/cgn2\_1/USPTO\_spool\_p/US09743209/runat\_02062004\_111815\_22122/app\_query.fasta\_1  
.711

-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09743209 @CGN\_1\_1\_6425 @runat\_02062004\_111815\_22122 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*

12: gb\_est3:\*  
 13: gb\_est4:\*  
 14: gb\_est5:\*  
 15: em\_estfun:\*  
 16: em\_estom:\*  
 17: em\_gss\_hum:\*  
 18: em\_gss\_inv:\*  
 19: em\_gss\_pln:\*  
 20: em\_gss\_vrt:\*  
 21: em\_gss\_fun:\*  
 22: em\_gss\_mam:\*  
 23: em\_gss\_mus:\*  
 24: em\_gss\_pro:\*  
 25: em\_gss\_rod:\*  
 26: em\_gss\_phg:\*  
 27: em\_gss\_vrl:\*  
 28: gb\_gss1:\*  
 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result |     |       | %     |        | Query |          | DB | ID       | Description |
|--------|-----|-------|-------|--------|-------|----------|----|----------|-------------|
|        | No. | Score | Match | Length | Score | Length   |    |          |             |
|        | 1   | 259.5 | 9.9   | 2209   | 11    | AY103777 |    | AY103777 | Zea mays    |
|        | 2   | 215.5 | 8.2   | 2368   | 28    | BH770685 |    | BH770685 | LLMGtag43   |
|        | 3   | 192.5 | 7.4   | 1124   | 14    | CK161710 |    | CK161710 | FGAS01428   |
|        | 4   | 187   | 7.1   | 4268   | 11    | BC050123 |    | BC050123 | Mus muscu   |
|        | 5   | 183.5 | 7.0   | 710    | 13    | CA131061 |    | CA131061 | SCBFRT106   |
|        | 6   | 183   | 7.0   | 1948   | 11    | AK076207 |    | AK076207 | Mus muscu   |
|        | 7   | 182.5 | 7.0   | 792    | 14    | CF554479 |    | CF554479 | GgW63 Inf   |
|        | 8   | 179.5 | 6.9   | 785    | 14    | CB643864 |    | CB643864 | OSJNEb04M   |
|        | 9   | 177.5 | 6.8   | 783    | 14    | CF642951 |    | CF642951 | D58_A05 F   |
|        | 10  | 176   | 6.7   | 938    | 14    | CK268111 |    | CK268111 | EST714189   |
|        | 11  | 175.5 | 6.7   | 949    | 14    | CK261193 |    | CK261193 | EST707271   |
|        | 12  | 175.5 | 6.7   | 1098   | 14    | CK162420 |    | CK162420 | FGAS01501   |
| c      | 13  | 173.5 | 6.6   | 691    | 14    | CF035102 |    | CF035102 | QCG14a05.   |
|        | 14  | 171.5 | 6.6   | 686    | 14    | CA266264 |    | CA266264 | SCAGLB204   |
|        | 15  | 171   | 6.5   | 624    | 13    | CA137709 |    | CA137709 | SCCCRT200   |
|        | 16  | 170.5 | 6.5   | 886    | 14    | CK271149 |    | CK271149 | EST717227   |
|        | 17  | 169.5 | 6.5   | 908    | 12    | BM816283 |    | BM816283 | HB105G02_   |
|        | 18  | 166.5 | 6.4   | 849    | 12    | BG583158 |    | BG583158 | EST484908   |
|        | 19  | 166.5 | 6.4   | 955    | 14    | CK274379 |    | CK274379 | EST720457   |
|        | 20  | 166   | 6.3   | 921    | 29    | CG346285 |    | CG346285 | OG0CO72TV   |
| c      | 21  | 165.5 | 6.3   | 694    | 14    | CF036180 |    | CF036180 | QCG28f07.   |
|        | 22  | 164.5 | 6.3   | 1041   | 13    | C23701   |    | C23701   | C23701 Dict |
|        | 23  | 164.5 | 6.3   | 3547   | 11    | BC030024 |    | BC030024 | Homo sapi   |
|        | 24  | 164   | 6.3   | 975    | 14    | CK263078 |    | CK263078 | EST709156   |
|        | 25  | 163.5 | 6.2   | 834    | 12    | BG582349 |    | BG582349 | EST484092   |
|        | 26  | 163.5 | 6.2   | 880    | 14    | CK270713 |    | CK270713 | EST716791   |
|        | 27  | 162.5 | 6.2   | 627    | 14    | CF645006 |    | CF645006 | K28_A02 F   |
|        | 28  | 162.5 | 6.2   | 667    | 14    | CF644832 |    | CF644832 | K26_A02 F   |
|        | 29  | 162   | 6.2   | 793    | 14    | CF554543 |    | CF554543 | GgW127 In   |